



(B)

Wed Nov 21 09:31:35 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]  
home/ruby/va/Molbio/carpanda/tempblast/pl.DNA35680 (1003 aa)

| Sequences producing High-scoring Segment Pairs: |            |   |      | Score | Match |
|---|------------|---|------|-------|-------|
| Pct   | E-val      |   |      |       |       |
| 1   | P_AAB65162 | Human PRO290 (UNQ253) protein sequence SE | 5247 | 1003  |       |
| 100   | 0.0        |   |      |       |       |
| 2   | P_AAB24058 | Human PRO290 protein sequence SEQ ID NO:7 | 5247 | 1003  |       |
| 100   | 0.0        |   |      |       |       |
| 3   | P_AAY66639 | Membrane-bound protein PRO290 - Homo sapi | 5235 | 1003  |       |
| 100   | 0.0        |   |      |       |       |
| 4   | P_AAB80418 | Gene #4 associated peptide #1 - Homo sapi | 5206 | 1003  |       |
| 97  | 0.0        |   |      |       |       |
| 5   | P_AAB80374 | Secreted protein encoded by gene #4 - Hom | 4810 | 927   |       |
| 97  | 0.0        |   |      |       |       |

>1 P\_AAB65162 Human PRO290 (UNQ253) protein sequence SEQ ID NO:33 - Homo  
(1003 aa) [1 seg]  
Score = 5247 (2025 bits), Expect = 0.0  
Identities = 1003/1003 (100%), Positives = 1003/1003 (100%), at 1,1-  
1003,1003

DNA35680 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

\*\*\*\*\*  
P\_AAB65162 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61  
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

\*\*\*\*\*  
P\_AAB65162 61  
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121  
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

\*\*\*\*\*  
P\_AAB65162 121  
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181  
AELETPMEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

\*\*\*\*\*  
P\_AAB65162 181  
AELETPMEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241  
IGYDFRRPLAQLEVLHRRFNLRSALELFFIDQANYFLNFPCKVGTPVSSPSQTPRPQ

\*\*\*\*\*  
P\_AAB65162 241  
IGYDFRRPLAQLEVLHRRFNLRSALELFFIDQANYFLNFPCKVGTPVSSPSQTPRPQ

DNA35680 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-1

\*\*\*\*\*  
P\_AAB65162 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKEHAQLVREKY

\*\*\*\*\*  
P\_AAB65162 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKEHAQLVREKY

DNA35680 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

\*\*\*\*\*  
P\_AAB65162 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481  
WQARLESPADVKELIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

\*\*\*\*\*  
P\_AAB65162 481  
WQARLESPADVKELIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEEEALNVFYCTYEGAVDLHDHVTDERERK

\*\*\*\*\*  
P\_AAB65162 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEEEALNVFYCTYEGAVDLHDHVTDERERK

DNA35680 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTV

\*\*\*\*\*  
P\_AAB65162 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTV

DNA35680 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

\*\*\*\*\*  
P\_AAB65162 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721  
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTCMVWRL

\*\*\*\*\*  
P\_AAB65162 721  
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTCMVWRL

DNA35680 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMVSGSEDGTVIIHTVRRGQFVAAL

\*\*\*\*\*  
P\_AAB65162 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMVSGSEDGTVIIHTVRRGQFVAAL

BLAST RESULTS B-2

DNA35680 841  
RPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

\*\*\*\*\*  
P\_AAB65162 841  
RPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901  
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

\*\*\*\*\*  
P\_AAB65162 901  
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

DNA35680 961 IVVVGQPSSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR  
\*\*\*\*\*  
P\_AAB65162 961 IVVVGQPSSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>2 P\_AAB24058 Human PRO290 protein sequence SEQ ID NO:7 - Homo sapiens.  
(1003 aa) [1 seg]  
Score = 5247 (2025 bits), Expect = 0.0  
Identities = 1003/1003 (100%), Positives = 1003/1003 (100%), at 1,1-  
1003,1003

DNA35680 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

\*\*\*\*\*  
P\_AAB24058 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61  
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMLK

\*\*\*\*\*  
P\_AAB24058 61  
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMLK

DNA35680 121  
LVPNHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

\*\*\*\*\*  
P\_AAB24058 121  
LVPNHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181  
AELETMPMAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

\*\*\*\*\*  
P\_AAB24058 181  
AELETMPMAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

\*\*\*\*\*  
P\_AAB24058 241  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

DNA35680 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-3

\*\*\*\*\*  
P\_AAB24058 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

\*\*\*\*\*  
P\_AAB24058 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

DNA35680 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

\*\*\*\*\*  
P\_AAB24058 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWASSPEDFIQ

\*\*\*\*\*  
P\_AAB24058 481  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWASSPEDFIQ

DNA35680 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYCYTYEGAVDLDHVTDERERK

\*\*\*\*\*  
P\_AAB24058 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYCYTYEGAVDLDHVTDERERK

DNA35680 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

\*\*\*\*\*  
P\_AAB24058 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

DNA35680 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

\*\*\*\*\*  
P\_AAB24058 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721  
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRD TTCMVWRL

\*\*\*\*\*  
P\_AAB24058 721  
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRD TTCMVWRL

DNA35680 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

\*\*\*\*\*  
P\_AAB24058 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

BLAST RESULTS B-A

DNA35680 841  
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

\*\*\*\*\*  
P\_AAB24058 841  
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901  
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

\*\*\*\*\*  
P\_AAB24058 901  
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

DNA35680 961 IVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR  
\*\*\*\*\*  
P\_AAB24058 961 IVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>3 P\_AAY66639 Membrane-bound protein PRO290 - Homo sapiens. (1004 aa) [1  
seg]

Score = 5235 (2021 bits), Expect = 0.0  
Identities = 1003/1004 (99%), Positives = 1003/1004 (99%), Gaps =  
1/1004 (0%), at 1,1-1003,1004

DNA35680 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

\*\*\*\*\*  
P\_AAY66639 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61  
GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

\*\*\*\*\*  
P\_AAY66639 61  
GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121  
LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

\*\*\*\*\*  
P\_AAY66639 121  
LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181  
AELETPMEEAELDEQREKLVLSAECQLTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

\*\*\*\*\*  
P\_AAY66639 181  
AELETPMEEAELDEQREKLVLSAECQLTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

\*\*\*\*\*  
P\_AAY66639 241  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

DNA35680 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

Blast Results B-5

\*\*\*\*\*  
P\_AAY66639 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

\*\*\*\*\*  
P\_AAY66639 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

DNA35680 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

\*\*\*\*\*  
P\_AAY66639 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

\*\*\*\*\*  
P\_AAY66639 481  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

\*\*\*\*\*  
P\_AAY66639 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

DNA35680 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

\*\*\*\*\*  
P\_AAY66639 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

DNA35680 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

\*\*\*\*\*  
P\_AAY66639 661  
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721  
KLLFSGGHWGSLRVLTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTTCMVWRL

\*\*\*\*\*  
P\_AAY66639 721  
KLLFSGGHWGSLRVLTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTTCMVWRL

DNA35680 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

\*\*\*\*\*  
P\_AAY66639 781  
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

Blast Results B-6

DNA35680 841  
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

\*\*\*\*\*

P\_AAY66639 841  
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901 ALTVTEDFVLLGTAQCALHI-  
LQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGK  
\*\*\*\*\*

\*\*\*\*\*

P\_AAY66639 901  
ALTVTEDFVLLGTAQCALHILLQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGK

DNA35680 960 LIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR  
\*\*\*\*\*

P\_AAY66639 961 LIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>4 P\_AAB80418 Gene #4 associated peptide #1 - Homo sapiens. (1041 aa) [1  
seg]

Score = 5206 (2009 bits), Expect = 0.0  
Identities = 1003/1033 (97%), Positives = 1003/1033 (97%), Gaps =  
30/1033 (2%), at 1,9-1003,1041

DNA35680 1  
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

\*\*\*\*\*

P\_AAB80418 9  
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61  
GLRYTAVLKQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

\*\*\*\*\*

P\_AAB80418 69  
GLRYTAVLKQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121  
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

\*\*\*\*\*

P\_AAB80418 129  
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181  
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

\*\*\*\*\*

P\_AAB80418 189  
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTTPVSSPSQTPRPQ

\*\*\*\*\*

P\_AAB80418 249  
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTTPVSSPSQTPRPQ

DNA35680 301  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-7

\*\*\*\*\*  
P\_AAB80418 309  
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSPKIGVVNPKHAQLVREKY

\*\*\*\*\*  
P\_AAB80418 369  
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSPKIGVVNPKHAQLVREKY

DNA35680 421  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

\*\*\*\*\*  
P\_AAB80418 429  
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

\*\*\*\*\*  
P\_AAB80418 489  
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

\*\*\*\*\*  
P\_AAB80418 549  
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

DNA35680 601  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAE---

\*\*\*\*\*  
P\_AAB80418 609  
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVVS

DNA35680 658 -----  
VTVSASGLLGTHSWLPYDRNISNYFSFSKDPTM

\*\*\*\*\*  
P\_AAB80418 669  
DGVFLVLALVPHRQPHSFITQGSPDLLVTVSASGLLGTHSWLPYDRNISNYFSFSKDPTM

DNA35680 691  
GSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLLSQLSCH

\*\*\*\*\*  
P\_AAB80418 729  
GSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLLSQLSCH

DNA35680 751  
LDVVTCLALDTCGIYLISGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVSCVAI

\*\*\*\*\*  
P\_AAB80418 789  
LDVVTCLALDTCGIYLISGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVSCVAI

BLAST RESULTS B-B



BLAST RESULTS B-9

DNA35680 811  
STELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGIIVVQSSAWE

\*\*\*\*\*

P\_AAB80418 849  
STELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGIIVVQSSAWE

DNA35680 871  
RPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA

\*\*\*\*\*

P\_AAB80418 909  
RPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA

DNA35680 931  
PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQV

\*\*\*\*\*

P\_AAB80418 969  
PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQV

DNA35680 991 SSGETEYNPTEAR

\*\*\*\*\*

P\_AAB80418 1029 SSGETEYNPTEAR

>5 P\_AAB80374 Secreted protein encoded by gene #4 - Homo sapiens. (957  
aa) [1 seg]

Score = 4810 (1857 bits), Expect = 0.0

Identities = 927/957 (96%), Positives = 927/957 (96%), Gaps = 30/957  
(3%), at 77,1-1003,957

DNA35680 77  
MALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNHHFDPHLEASAL

\*\*\*\*\*

P\_AAB80374 1  
MALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNHHFDPHLEASAL

DNA35680 137  
RDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETPMEAAELDEQR

\*\*\*\*\*

P\_AAB80374 61  
RDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETPMEAAELDEQR

DNA35680 197  
EKLVLSAECQLVTVVAVVPGLEVTQNVYFYDGS TERVETEEGIGYDFRRPLAQLREXH

\*\*\*\*\*

P\_AAB80374 121  
EKLVLSAECQLVTVVAVVPGLEVTQNVYFYDGS TERVETEEGIGYDFRRPLAQLREXH

DNA35680 257  
LRRFNLRRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQPGPIPPHTQVRNQVYS

\*\*\*\*\*

P\_AAB80374 181  
LRRFNLRRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQPGPIPPHTQVRNQVYS

DNA35680 317  
WLLRLRPSPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGR TYNDLSQYP

```

*****
P_AAB80374 241
WLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGR TYNDLSQYP

DNA35680 377
VFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFHYG

*****
P_AAB80374 301
VFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFHYG

DNA35680 437
THYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP

*****
P_AAB80374 361
THYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP

DNA35680 497
EFFYFPDFLENQNGFDLGCLQLTNEKVG DVVLPPWASSPEDFIQQHRQALESEYVSAHLH

*****
P_AAB80374 421
EFFYFPDFLENQNGFDLGCLQLTNEKVG DVVLPPWASSPEDFIQQHRQALESEYVSAHLH

DNA35680 557
EWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDL DHVTDERERKALEGIISNFGQTPCQL

*****
P_AAB80374 481
EWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDL DHVTDERERKALEGIISNFGQTPCQL

DNA35680 617
LKEPHPTRLSAEEAAHRLARLDTNPSIFQH LDELKAFFAE-----
*****
P_AAB80374 541
LKEPHPTRLSAEEAAHRLARLDTNPSIFQH LDELKAFFAEVVS DGVPLVLALVPHRQPH

DNA35680 658 -----
VTVSASGLLGTHSWLPYDRNISNYFSFSKDPTMG SHKTQRLLSGPWVPG

*****
P_AAB80374 601
SFITQGSPDLLVTVSASGLLGTHSWLPYDRNISNYFSFSKDPTMG SHKTQRLLSGPWVPG

DNA35680 707
SGVSGQALAVAPDGKLLFSGGHW DGLRV TALPRGKLLSQLSCHLDVVTCLALDTCGIYL

*****
P_AAB80374 661
SGVSGQALAVAPDGKLLFSGGHW DGLRV TALPRGKLLSQLSCHLDVVTCLALDTCGIYL

DNA35680 767
ISGSRDTTCMVWRL LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDM AVSGSEDGTV

*****
P_AAB80374 721
ISGSRDTTCMVWRL LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDM AVSGSEDGTV

DNA35680 827

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BLAST RESULTS B-10

IIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVN

\*\*\*\*\*

P\_AAB80374 781

IIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVN

DNA35680 887

GKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTK

\*\*\*\*\*

P\_AAB80374 841

GKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTK

DNA35680 947

ERSHVLVGLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

\*\*\*\*\*

P\_AAB80374 901

ERSHVLVGLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

Blast Results B-11